

SEQUENCE LISTING

<110> Japan Tobacco, Inc.

<120> Monoclonal Antibody Against Connective Tissue Growth Factor
and Medicinal Uses Thereof

<130> J1-009PCT

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<150> JP P1997-367699

<151> 1997-12-25

<150> JP P1998-356183

<151> 1998-12-15

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<170> PatentIn Ver. 2.0

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 Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu Gly Glu
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 Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu Phe Cys
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 Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Pro Ala Lys
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 Asp Gly Ala Pro Cys Val Phe Gly Gly Ser Val Tyr Arg Ser Gly Glu
 100 105 110
 Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp Gly Ala
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 Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys Cys Glu
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 Glu Trp Val Cys Asp Glu Pro Lys Asp Arg Thr Val Val Gly Pro Ala
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 Pro Gly Gly Ser Leu Lys Thr Ser Pro Val Gln Pro Leu Asp Ser Thr
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 Phe Ser Asn Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly
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 Trp Ser Gly Leu Ala Val Leu Lys Ala Lys Leu Met Val Gly His Thr
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 gac tac gct gca ccc gtg aaa ggc aga ttc acc atc tca aga gat gat 288
 Asp Tyr Ala Ala Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp
 85 90 95
 tca aaa aac acg ctg tat ctg caa atg aac agc ctg aaa acc gag gac 336
 Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp
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 Thr Ala Val Tyr Tyr Cys Thr Thr Lys Trp Val Ala Thr Asp Tyr Phe
 115 120 125
 gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc tca gcc tcc acc 432
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Trp Ser Gly Leu Ala Val Leu Lys Ala Lys Leu Met Val Gly His Thr
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Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp
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Lys Gly Pro Ser
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Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Phe Trp Leu His Leu	
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Ser Pro Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly	
50 55 60	
ctt gag tgg atg gga tgg atc aac cct aac agt agt ggc aca cac tat	240
Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Ser Gly Thr His Tyr	
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Ala Gln Met Phe Gln Gly Arg Val Thr Val Thr Arg Asp Thr Ser Ile	
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Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala	
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gtg tat tac tgt gcg aga gag ggg ata gca gca gct gcc atc tac ggt	384
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atg gac gtc tgg ggc caa ggg acc acg gtc acc gtc tcc tca gcc tcc	432
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Ala Gln Met Phe Gln Gly Arg Val Thr Val Thr Arg Asp Thr Ser Ile	
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Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala	

100 105 110

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Thr Glu Leu Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
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Glu Trp Met Gly Ser Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala	
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Gln Lys Phe Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp	
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aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
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Tyr Tyr Cys Ala Thr Ser Thr Val Val Thr Pro Trp Tyr Phe Asp Tyr
115 120 125

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Glu Trp Met Gly Ser Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala
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Gln Lys Phe Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp
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Thr His Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
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cct ggg gcc tca gtg aag gtc tcc tgc aag gtt tcc gga tac acc ctc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu	
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Glu Trp Met Gly Ser Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala	
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 Thr Glu Leu Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
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 65 70 75 80
 Gln Lys Phe Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp
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 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
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 ggt cct gtc cca ggt gca gct gca gga gtc ggg ccc agg act ggt gaa 96
 Gly Pro Val Pro Gly Ala Ala Ala Gly Val Gly Pro Arg Thr Gly Glu
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 gcc ttc aca gac cct gtc ctc acc tgc act gtc tct ggt ggc tcc atc 144
 Ala Phe Thr Asp Pro Val Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
 35 40 45

123

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 ggc ctg gag tgg att ggg tac atc tat tac agt ggg agc acc tac tac 240
 Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr
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 Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
 85 90 95
 aac cag ttc tcc ctg aag ctg agc tct gtg act gcc gcg gac acg gcc 336
 Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
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 Val Tyr Tyr Cys Ala Ser Tyr Tyr Tyr Asp Ser Gly Gly Tyr Tyr Asp
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 Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr
 65 70 75 80
 Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
 85 90 95
 Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
 100 105 110
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 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
 1 5 10 15

ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct 96
 Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
 20 25 30

gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag act 144
 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Thr
 35 40 45

gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag 192
 Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
 50 55 60

aaa cca gga cag cct cct aag ctg ctc att tac tgg gca tct acc cgg 240
 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 65 70 75 80

gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat 288
 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 85 90 95

ttc act ctc acc atc agc agc ctg cag gct gac gat gtg gca gtt tat 336
 Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Asp Asp Val Ala Val Tyr
 100 105 110

tac tgt cag caa tat tat agt act cct ccg tgg acg ttc ggc caa ggg 384
 Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Trp Thr Phe Gly Gln Gly
 115 120 125

acc aag gtg gaa atc aaa cga act gtg gct gca cca tct 423

Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
 130 135 140

<210> 16
 <211> 141
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
 1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
 20 25 30

Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Thr
 35 40 45

Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
 50 55 60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 85 90 95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Asp Asp Val Ala Val Tyr
 100 105 110

Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Trp Thr Phe Gly Gln Gly
 115 120 125

Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
 130 135 140

<210> 17
 <211> 420
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(420)

<220>
 <221> sig_peptide
 <222> (1)..(60)

<220>
 <221> V_region
 <222> (61)..(364)

<400> 17
 atg aag gat ctg ctc agc ttc ctg ggg ctg cta atg ctc tgg ata cct 48
 Met Lys Asp Leu Leu Ser Phe Leu Gly Leu Leu Met Leu Trp Ile Pro

1	5	10	15	
gga tcc agt gca gat att gtc atg acc cag acg cca ctc ttc tgt ccg				96
Gly Ser Ser Ala Asp Ile Val Met Thr Gln Thr Pro Leu Phe Cys Pro	20	25	30	
tca ccc ctg gac agc cga gcc tcc atc tcc tgc aag tct ggt ctg agc				144
Ser Pro Leu Asp Ser Arg Ala Ser Ile Ser Cys Lys Ser Gly Leu Ser	35	40	45	
ctc ctg cac agt gat gga aag acc tat ttg cat tgg tac ctg cag aag				192
Leu Leu His Ser Asp Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys	50	55	60	
cca ggc cag cct cca cag ctc ctg atc tat gag agt ttc caa ccg gtt				240
Pro Gly Gln Pro Pro Gln Leu Leu Ile Tyr Glu Ser Phe Gln Pro Val	65	70	75	80
ctc ctg gag tgc cag ata ggc tca gtg gca gcg ggt cag gac aga ttt				288
Leu Leu Glu Cys Gln Ile Gly Ser Val Ala Ala Gly Gln Asp Arg Phe	85	90	95	
cac act gaa aat cag ccg ggt gga agg ctg agg aat gtt ggg gtt tat				336
His Thr Glu Asn Gln Pro Gly Gly Arg Leu Arg Asn Val Gly Val Tyr	100	105	110	
tac tgc atg caa agt tta cag ctt ccg ctc act ttc ggc gga ggg acc				384
Tyr Cys Met Gln Ser Leu Gln Leu Pro Leu Thr Phe Gly Gly Gly Thr	115	120	125	
aag gtg gag atc aaa cga act gtg gct gca cca tct				420
Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser	130	135	140	

<210> 18
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Lys Asp Leu Leu Ser Phe Leu Gly Leu Leu Met Leu Trp Ile Pro
 1 5 10 15
 Gly Ser Ser Ala Asp Ile Val Met Thr Gln Thr Pro Leu Phe Cys Pro
 20 25 30
 Ser Pro Leu Asp Ser Arg Ala Ser Ile Ser Cys Lys Ser Gly Leu Ser
 35 40 45
 Leu Leu His Ser Asp Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys
 50 55 60
 Pro Gly Gln Pro Pro Gln Leu Leu Ile Tyr Glu Ser Phe Gln Pro Val
 65 70 75 80
 Leu Leu Glu Cys Gln Ile Gly Ser Val Ala Ala Gly Gln Asp Arg Phe
 85 90 95

His Thr Glu Asn Gln Pro Gly Gly Arg Leu Arg Asn Val Gly Val Tyr
 100 105 110

Tyr Cys Met Gln Ser Leu Gln Leu Pro Leu Thr Phe Gly Gly Gly Thr
 115 120 125

Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
 130 135 140

<210> 19
 <211> 405
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(405)

<220>
 <221> sig_peptide
 <222> (1)..(66)

<220>
 <221> V_region
 <222> (67)..(353)

<400> 19
 atg gac atg agg gtc cct gct cag ctc ctg ggg ctc ctg ctg ctc tgg 48
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15

ctc tca ggt gcc aga tgt gac atc cag atg acc cag tct cca tcc ttc 96
 Leu Ser Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Phe
 20 25 30

cct gtc tgc atc tgt agg aga cag agt cac cat cac ttg cca ggc gag 144
 Pro Val Cys Ile Cys Arg Arg Gln Ser His His His Leu Pro Gly Glu
 35 40 45

tca gga cat tca cca cta ttt aaa ttg gta tca gca gaa acc agg gaa 192
 Ser Gly His Ser Pro Leu Phe Lys Leu Val Ser Ala Glu Thr Arg Glu
 50 55 60

agc cct aag ctc ctg atc tac gat gca tcc aat ttg gaa aca ggg tcc 240
 Ser Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Ser
 65 70 75 80

cat cac ggt tca gtg gaa gtg gat ctg gga cag att tta ctt tca cca 288
 His His Gly Ser Val Glu Val Asp Leu Gly Gln Ile Leu Leu Ser Pro
 85 90 95

tca gca gcc tgc agc tct gaa gat att gca aca tat tac tgt caa cag 336
 Ser Ala Ala Cys Ser Ser Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110

tat aat aat ctc atc acc ttc ggc caa ggg aca cga ctg gag att aaa 384
 Tyr Asn Asn Leu Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys

115 120 125 405
cga act gtg gct gca cca tct
Arg Thr Val Ala Ala Pro Ser
130 135

<210> 20
<211> 135
<212> PRT
<213> Homo sapiens

<400> 20
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp
1 5 10 15
Leu Ser Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Phe
20 25 30
Pro Val Cys Ile Cys Arg Arg Gln Ser His His His Leu Pro Gly Glu
35 40 45
Ser Gly His Ser Pro Leu Phe Lys Leu Val Ser Ala Glu Thr Arg Glu
50 55 60
Ser Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Ser
65 70 75 80
His His Gly Ser Val Glu Val Asp Leu Gly Gln Ile Leu Leu Ser Pro
85 90 95
Ser Ala Ala Cys Ser Ser Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln
100 105 110
Tyr Asn Asn Leu Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
115 120 125
Arg Thr Val Ala Ala Pro Ser
130 135

<210> 21
<211> 387
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(387)

<220>
<221> sig_peptide
<222> (1)..(47)
<223> Initiation codon and a portion of a signal
sequence are lacked.

<220>
<221> V_region

<222> (48) .. (335)

<400> 21

gat	agg	gtc	cta	ggg	gtc	ctg	atg	gtt	ggg	ttt	tcg	gtg	ccg	gat	gag	48
Asp	Arg	Val	Leu	Gly	Val	Leu	Met	Val	Gly	Phe	Ser	Val	Pro	Asp	Glu	
1				5					10					15		
aac	atc	cag	atg	acc	cag	tat	cca	tct	ccc	tgt	ctg	cat	acc	tgt	agg	96
Asn	Ile	Gln	Met	Thr	Gln	Tyr	Pro	Ser	Pro	Cys	Leu	His	Thr	Cys	Arg	
			20					25					30			
aga	cag	agt	cac	cat	cac	ttg	cca	gag	cga	gct	cag	gac	att	cac	cac	144
Arg	Gln	Ser	His	His	His	Leu	Pro	Glu	Arg	Ala	Gln	Asp	Ile	His	His	
			35				40					45				
tat	cta	aat	tgg	tat	cag	cag	aaa	cca	ggg	aaa	gcc	cta	agc	tct	gat	192
Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Leu	Ser	Ser	Asp	
	50					55					60					
cta	cga	tgc	atc	caa	ttt	gga	aac	agg	gtc	cca	tca	cgg	ttc	agt	gga	240
Leu	Arg	Cys	Ile	Gln	Phe	Gly	Asn	Arg	Val	Pro	Ser	Arg	Phe	Ser	Gly	
	65				70				75						80	
agt	gga	tct	ggg	aca	gat	tct	act	tca	cca	tca	gca	gcc	tgc	agc	tct	288
Ser	Gly	Ser	Gly	Thr	Asp	Ser	Thr	Ser	Pro	Ser	Ala	Ala	Cys	Ser	Ser	
				85					90					95		
gaa	gat	att	gca	aca	tat	tac	tgt	caa	cag	tat	aat	aat	ctc	atc	acc	336
Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Asn	Asn	Leu	Ile	Thr	
			100					105					110			
ttc	ggc	caa	ggg	aca	cga	ctg	gag	att	aaa	cga	act	gtg	gct	gca	cca	384
Phe	Gly	Gln	Gly	Thr	Arg	Leu	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	
		115					120					125				
tct																387
Ser																

<210> 22

<211> 129

<212> PRT

<213> Homo sapiens

<400> 22

Asp	Arg	Val	Leu	Gly	Val	Leu	Met	Val	Gly	Phe	Ser	Val	Pro	Asp	Glu	
1				5					10					15		
Asn	Ile	Gln	Met	Thr	Gln	Tyr	Pro	Ser	Pro	Cys	Leu	His	Thr	Cys	Arg	
			20					25					30			
Arg	Gln	Ser	His	His	His	Leu	Pro	Glu	Arg	Ala	Gln	Asp	Ile	His	His	
			35				40					45				
Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Leu	Ser	Ser	Asp	
	50					55					60					
Leu	Arg	Cys	Ile	Gln	Phe	Gly	Asn	Arg	Val	Pro	Ser	Arg	Phe	Ser	Gly	

130

65		70		75		80
Ser Gly Ser Gly Thr Asp Ser Thr Ser Pro Ser Ala Ala Cys Ser Ser						
		85		90		95
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Asn Leu Ile Thr						
	100		105		110	
Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala Pro						
	115		120		125	

Ser

<210> 23
 <211> 411
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(411)

<220>
 <221> sig_peptide
 <222> (1)..(66)

<220>
 <221> V_region
 <222> (67)..(356)

<400> 23	
atg gac atg agg gtc cct gct cag ctc ctg ggg ctc ctg ctg ctc tgg	48
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp	
1 5 10 15	
ctc tca ggt gcc aga tgt gac atc cag atg acc cag tct cca tcc tcc	96
Leu Ser Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser	
20 25 30	
ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gca agt	144
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser	
35 40 45	
cag agc att agc agc tat tta aat tgg tat cag cag aaa cca ggg aaa	192
Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys	
50 55 60	
gcc cct aag ctc ctg att tat gct gca tcc agt ttg caa agt ggg tcc	240
Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ser	
65 70 75 80	
cat caa ggt tca gtg gca gtg gat tat gcg aca gat ttc cat ttc tca	288
His Gln Gly Ser Val Ala Val Asp Tyr Ala Thr Asp Phe His Phe Ser	
85 90 95	
cca tca gca gtt tgc cac ctg acg att ttg caa ctt act act gtc cac	336
Pro Ser Ala Val Cys His Leu Thr Ile Leu Gln Leu Thr Thr Val His	

131

100 105 110
 aga gtt aca gta tcc cat tca ctt tcg gcc ctg ggg acc aaa gtg gat 384
 Arg Val Thr Val Ser His Ser Leu Ser Ala Leu Gly Thr Lys Val Asp
 115 120 125

agc aaa cga act gtg gct gca cca tct 411
 Ser Lys Arg Thr Val Ala Ala Pro Ser
 130 135

<210> 24
 <211> 137
 <212> PRT
 <213> Homo sapiens

<400> 24
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15
 Leu Ser Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
 20 25 30
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 35 40 45
 Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
 50 55 60
 Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ser
 65 70 75 80
 His Gln Gly Ser Val Ala Val Asp Tyr Ala Thr Asp Phe His Phe Ser
 85 90 95
 Pro Ser Ala Val Cys His Leu Thr Ile Leu Gln Leu Thr Thr Val His
 100 105 110
 Arg Val Thr Val Ser His Ser Leu Ser Ala Leu Gly Thr Lys Val Asp
 115 120 125
 Ser Lys Arg Thr Val Ala Ala Pro Ser
 130 135

<210> 25
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
 synthesized adaptor sequence

<220>
 <221> misc_difference
 <222> (1)..(27)

132

<400> 25
ccatcctaatac gactcact atagggc

27

<210> 26
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<220>
<221> primer_bind
<222> (1)..(25)

<400> 26
ccagggccgc tgtgctctcg gaggt

25

<210> 27
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<220>
<221> primer_bind
<222> (1)..(23)

<400> 27
gggggtcagg ctggaactga gga

23